

7.0 SEQUENCE LISTING

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Baum, James A.
Gilmer, Amy Jelen
Mettus, Anne-Marie Light

(ii) TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
LEPIDOPTERAN-ACTIVE- δ -ENDOTOXINS

(iii) NUMBER OF SEQUENCES: 76

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Arnold, White & Durkee
(B) STREET: P.O. Box 4433
(C) CITY: Houston
(D) STATE: Texas
(E) COUNTRY: USA
(F) ZIP: 77210

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unknown
(B) FILING DATE:
(C) CLASSIFICATION: Unknown

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/757,536
(B) FILING DATE: 27-NOV-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kitchell, Barbara S.
(B) REGISTRATION NUMBER: 33,928
(C) REFERENCE/DOCKET NUMBER: MECO:206

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 512/418-3000
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3567 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10	ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT	48
	Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser	
	1 5 10 15	
15	AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT	96
	Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	
	20 25 30	
20	TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC	144
	Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
	35 40 45	
25	TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG	192
	Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
	50 55 60	
30	GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA	240
	Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
	65 70 75 80	
35	CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT	288
	Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
	85 90 95	
40	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA	336
	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
	100 105 110	
45	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA	384
	Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg	
	115 120 125	
50	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT	432
	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	
	130 135 140	
55	CCT TCG TTT GCA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT	480
	Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	
	145 150 155 160	
60	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT	528
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	
	165 170 175	

	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT	576
	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	
	180 185 190	
5	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT	624
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	
	195 200 205	
10	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT	672
	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp	
	210 215 220	
15	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA	720
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	
	225 230 235 240	
20	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT	768
	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	
	245 250 255	
25	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT	816
	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	
	260 265 270	
30	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC	864
	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	
	275 280 285	
35	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG	912
	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	
	290 295 300	
40	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT	960
	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	
	305 310 315 320	
45	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC	1008
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn	
	325 330 335	
50	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA	1056
	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg	
	340 345 350	
55	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT	1104
	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr	
	355 360 365	
60	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT	1152
	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg	
	370 375 380	

	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT	1200
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr	
	385 390 395 400	
5	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT	1248
	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp	
	405 410 415	
10	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA	1296
	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala	
	420 425 430	
15	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA	1344
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val	
	435 440 445	
20	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA	1392
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	
	450 455 460	
25	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG	1440
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465 470 475 480	
30	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT	1488
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
	485 490 495	
35	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT	1536
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	
	500 505 510	
40	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT	1584
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
	515 520 525	
45	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG	1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530 535 540	
50	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA	1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545 550 555 560	
55	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT	1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565 570 575	
60	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA	1776
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580 585 590	

	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT	1824
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595 600 605	
5	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT	1872
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610 615 620	
10	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT	1920
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625 630 635 640	
15	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA	1968
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
	645 650 655	
	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG	2016
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
	660 665 670	
20	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG	2064
	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675 680 685	
25	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA	2112
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690 695 700	
30	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT	2160
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705 710 715 720	
35	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG	2208
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
	725 730 735	
40	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA	2256
	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
	740 745 750	
	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC	2304
	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
	755 760 765	
45	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT	2352
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
	770 775 780	
50	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC	2400
	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	
	785 790 795 800	

	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT	2448
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	
	805 810 815	
5	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT	2496
	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	
	820 825 830	
10	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT	2544
	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	
	835 840 845	
15	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC	2592
	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly	
	850 855 860	
20	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA	2640
	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu	
	865 870 875 880	
25	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC	2688
	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp	
	885 890 895	
30	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA	2736
	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala	
	900 905 910	
35	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA	2784
	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu	
	915 920 925	
40	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT	2832
	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val	
	930 935 940	
45	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT	2880
	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly	
	945 950 955 960	
50	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG	2928
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala	
	965 970 975	
55	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT	2976
	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn	
	980 985 990	
60	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG	3024
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	
	995 1000 1005	

	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA	3072
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu	
	1010 1015 1020	
5	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT	3120
	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	
	1025 1030 1035 1040	
10	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT	3168
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	
	1045 1050 1055	
15	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA	3216
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	
	1060 1065 1070	
	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG	3264
	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly	
	1075 1080 1085	
20	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT	3312
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr	
	1090 1095 1100	
25	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA	3360
	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser	
	1105 1110 1115 1120	
30	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT	3408
	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys	
	1125 1130 1135	
35	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT	3456
	Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr	
	1140 1145 1150	
40	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT	3504
	Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile	
	1155 1160 1165	
	GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA	3552
	Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu	
	1170 1175 1180	
45	CTC CTT ATG GAG GAA	3567
	Leu Leu Met Glu Glu	
	1185	

50 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
1 5 10 15
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
20 25 30
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
35 40 45
Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
50 55 60
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65 70 75 80
Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
85 90 95
Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
100 105 110
Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
115 120 125
Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
130 135 140
Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145 150 155 160
Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
165 170 175
Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
180 185 190
Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
195 200 205
Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
210 215 220
Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
225 230 235 240
Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
245 250 255

	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	
	260	265 270
5	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	
	275	280 285
	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	
	290	295 300
10	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	
	305	310 315 320
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn	
		325 330 335
15	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg	
	340	345 350
	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr	
20	355	360 365
	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg	
	370	375 380
25	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr	
	385	390 395 400
	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp	
		405 410 415
30	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala	
	420	425 430
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val	
35	435	440 445
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	
	450	455 460
40	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465	470 475 480
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
		485 490 495
45	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	
	500	505 510
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
50	515	520 525
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530	535 540

	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545	550 555 560
5	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565	570 575
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580	585 590
10	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595	600 605
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610	615 620
15	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625	630 635 640
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
20	645	650 655
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
	660	665 670
25	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675	680 685
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690	695 700
30	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705	710 715 720
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
35	725	730 735
	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
	740	745 750
40	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
	755	760 765
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
45	770	775 780
	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	
	785	790 795 800
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	
50	805	810 815
	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	
	820	825 830

Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
 835 840 845
 5 Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
 850 855 860
 His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
 865 870 875 880
 10 Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
 885 890 895
 Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
 900 905 910
 15 Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
 915 920 925
 Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
 930 935 940
 20 His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
 945 950 955 960
 25 Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
 965 970 975
 Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
 980 985 990
 30 Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
 995 1000 1005
 Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
 1010 1015 1020
 35 Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1025 1030 1035 1040
 40 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055
 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070
 45 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085
 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 50 1090 1095 1100
 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120

Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135

5 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150

Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

10 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

Leu Leu Met Glu Glu
 1185

15

(2) INFORMATION FOR SEQ ID NO:3:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..3567

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT 48
 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15

35 AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT 96
 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30

40 TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC 144
 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45

45 TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG 192
 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
 50 55 60

GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA 240
 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80

50 CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT 288
 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
 85 90 95

	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA	336
	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
	100 105 110	
5	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA	384
	Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg	
	115 120 125	
10	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT	432
	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	
	130 135 140	
15	CCT TCG TTT GAC ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT	480
	Pro Ser Phe Asp Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	
	145 150 155 160	
20	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT	528
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	
	165 170 175	
25	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT	576
	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	
	180 185 190	
30	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT	624
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	
	195 200 205	
35	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT	672
	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp	
	210 215 220	
40	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA	720
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	
	225 230 235 240	
45	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT	768
	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	
	245 250 255	
50	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT	816
	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	
	260 265 270	
55	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC	864
	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	
	275 280 285	
60	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG	912
	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	
	290 295 300	

	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT	960
	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	
	305 310 315 320	
5	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC	1008
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn	
	325 330 335	
10	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA	1056
	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg	
	340 345 350	
15	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT	1104
	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr	
	355 360 365	
20	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT	1152
	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg	
	370 375 380	
25	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT	1200
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr	
	385 390 395 400	
30	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT	1248
	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp	
	405 410 415	
35	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA	1296
	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala	
	420 425 430	
40	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA	1344
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val	
	435 440 445	
45	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA	1392
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	
	450 455 460	
50	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG	1440
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465 470 475 480	
55	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT	1488
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
	485 490 495	
60	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT	1536
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	
	500 505 510	

	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT	1584
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
	515 520 525	
5	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG	1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530 535 540	
10	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA	1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545 550 555 560	
15	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT	1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565 570 575	
20	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA	1776
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580 585 590	
25	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT	1824
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595 600 605	
30	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT	1872
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610 615 620	
35	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT	1920
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625 630 635 640	
40	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA	1968
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
	645 650 655	
45	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG	2016
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
	660 665 670	
50	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG	2064
	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675 680 685	
55	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA	2112
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690 695 700	
60	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT	2160
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705 710 715 720	

	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG	2208
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
	725 730 735	
5	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA	2256
	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
	740 745 750	
10	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC	2304
	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
	755 760 765	
15	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT	2352
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
	770 775 780	
20	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC	2400
	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	
	785 790 795 800	
25	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT	2448
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	
	805 810 815	
30	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT	2496
	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	
	820 825 830	
35	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT	2544
	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	
	835 840 845	
40	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC	2592
	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly	
	850 855 860	
45	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA	2640
	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu	
	865 870 875 880	
50	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC	2688
	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp	
	885 890 895	
55	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA	2736
	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala	
	900 905 910	
60	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA	2784
	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu	
	915 920 925	

	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT	2832
	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val	
	930 935 940	
5	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT	2880
	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly	
	945 950 955 960	
10	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG	2928
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala	
	965 970 975	
15	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT	2976
	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn	
	980 985 990	
	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG	3024
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	
	995 1000 1005	
20	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA	3072
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu	
	1010 1015 1020	
25	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT	3120
	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	
	1025 1030 1035 1040	
30	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT	3168
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	
	1045 1050 1055	
35	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA	3216
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	
	1060 1065 1070	
40	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG	3264
	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly	
	1075 1080 1085	
45	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT	3312
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr	
	1090 1095 1100	
50	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA	3360
	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser	
	1105 1110 1115 1120	
50	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT	3408
	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys	
	1125 1130 1135	

GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT 3456
 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150

5 GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT 3504
 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

10 GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA 3552
 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

15 CTC CTT ATG GAG GAA 3567
 Leu Leu Met Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO:4:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1189 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15

Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30

35 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45

Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
 50 55 60

40 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80

45 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
 85 90 95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
 100 105 110

50 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
 115 120 125

Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
 130 135 140

Pro Ser Phe Asp Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
 145 150 155 160

5 Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
 165 170 175

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
 180 185 190

10 Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
 195 200 205

Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
 210 215 220

15 Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
 225 230 235 240

20 Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
 245 250 255

Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
 260 265 270

25 Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
 275 280 285

Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
 290 295 300

30 Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
 305 310 315 320

35 Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
 325 330 335

Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
 340 345 350

40 Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
 355 360 365

Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
 370 375 380

45 Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
 385 390 395 400

50 Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
 405 410 415

Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
 420 425 430

	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val	
	435	440 445
5	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	
	450	455 460
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465	470 475 480
10	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
	485	490 495
15	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn -	
	500	505 510
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
	515	520 525
20	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530	535 540
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545	550 555 560
25	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565	570 575
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580	585 590
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595	600 605
35	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610	615 620
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625	630 635 640
40	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
	645	650 655
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
45	660	665 670
	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675	680 685
50	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690	695 700
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705	710 715 720

	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	Thr	Leu	Pro	Gly	Thr	Val	Asp	Glu	
					725					730					735		
5	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	
					740				745					750			
	Ala	Tyr	Thr	Arg	Tyr	Glu	Leu	Arg	Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	
					755				760					765			
10	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	Asn	Ala	Lys	His	Glu	Ile	Val	Asn	
					770				775					780			
	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	Pro	Leu	Ser	Ala	Gln	Ser	Pro	Ile	
15					785				790					795		800	
	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	
					805					810					815		
20	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	Asp	Gly	Glu	Lys	Cys	Ala	His	His	
					820				825						830		
	Ser	His	His	Phe	Thr	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	
					835				840					845			
25	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	
					850				855					860			
	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Leu	Glu	Glu	Lys	Pro	Leu	Leu	
					865				870					875		880	
	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	
					885					890					895		
30	Lys	Arg	Glu	Lys	Leu	Gln	Leu	Glu	Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	
					900					905					910		
	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe	Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	
					915				920					925			
40	Gln	Val	Asp	Thr	Asn	Ile	Ala	Met	Ile	His	Ala	Ala	Asp	Lys	Arg	Val	
					930				935					940			
	His	Arg	Ile	Arg	Glu	Ala	Tyr	Leu	Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	
45					945				950					955		960	
	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu	Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	
					965					970					975		
50	Tyr	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	
					980					985				990			
	Asn	Gly	Leu	Leu	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Glu	Glu	
					995				1000					1005			

Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
 1010 1015 1020

5 Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1025 1030 1035 1040

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055

10 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070

15 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100

20 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120

Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150

Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

Leu Leu Met Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3567 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT	48
	Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser	
	1 5 10 15	
5	AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT	96
	Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	
	20 25 30	
10	TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC	144
	Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
	35 40 45	
15	TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG	192
	Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
	50 55 60	
20	GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA	240
	Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
	65 70 75 80	
25	CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT	288
	Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
	85 90 95	
30	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA	336
	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
	100 105 110	
35	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA	384
	Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg	
	115 120 125	
40	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT	432
	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	
	130 135 140	
45	CCT TCG TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT	480
	Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	
	145 150 155 160	
50	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT	528
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	
	165 170 175	
55	TTT GGA GAA GCA TGG GGG TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT	576
	Phe Gly Glu Ala Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	
	180 185 190	
60	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT	624
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	
	195 200 205	

	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT	ACG TAT CAA GAT	672
	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp		
	210 215 220		
5	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA	720	
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu		
	225 230 235 240		
10	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT	768	
	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile		
	245 250 255		
15	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT	816	
	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile		
	260 265 270		
20	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC	864	
	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn		
	275 280 285		
25	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG	912	
	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu		
	290 295 300		
30	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT	960	
	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe		
	305 310 315 320		
35	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC	1008	
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn		
	325 330 335		
40	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA	1056	
	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg		
	340 345 350		
45	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT	1104	
	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr		
	355 360 365		
50	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT	1152	
	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg		
	370 375 380		
55	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT	1200	
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr		
	385 390 395 400		
60	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT	1248	
	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp		
	405 410 415		

	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA	1296
	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala	
	420 425 430	
5	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA	1344
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val	
	435 440 445	
10	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA	1392
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	
	450 455 460	
15	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG	1440
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465 470 475 480	
20	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT	1488
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
	485 490 495	
25	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT	1536
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	
	500 505 510	
30	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT	1584
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
	515 520 525	
35	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG	1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530 535 540	
40	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA	1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545 550 555 560	
45	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT	1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565 570 575	
50	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA	1776
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580 585 590	
55	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT	1824
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595 600 605	
60	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT	1872
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610 615 620	

	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT	1920
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625 630 635 640	
5	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA	1968
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
	645 650 655	
10	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG	2016
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
	660 665 670	
15	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG	2064
	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675 680 685	
20	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA	2112
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690 695 700	
25	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT	2160
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705 710 715 720	
30	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG	2208
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
	725 730 735	
35	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA	2256
	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
	740 745 750	
40	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC	2304
	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
	755 760 765	
45	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT	2352
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
	770 775 780	
50	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC	2400
	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	
	785 790 795 800	
55	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT	2448
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	
	805 810 815	
60	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT	2496
	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	
	820 825 830	

	TCC CAT CAT TTC ACC TTG [*] GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT	2544
	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	
	835 840 845	
5	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC	2592
	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly	
	850 855 860	
10	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA	2640
	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu	
	865 870 875 880	
15	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC	2688
	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp	
	885 890 895	
	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA	2736
	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala	
	900 905 910	
20	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA	2784
	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu	
	915 920 925	
25	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT	2832
	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val	
	930 935 940	
30	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT	2880
	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly	
	945 950 955 960	
35	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG	2928
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala	
	965 970 975	
40	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT	2976
	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn	
	980 985 990	
	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG	3024
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	
	995 1000 1005	
45	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA	3072
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu	
	1010 1015 1020	
50	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT	3120
	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	
	1025 1030 1035 1040	

20
25
30
35
40

	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT	3168
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	
	1045 1050 1055	
5	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA	3216
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	
	1060 1065 1070	
10	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG	3264
	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly	
	1075 1080 1085	
15	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT	3312
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr	
	1090 1095 1100	
	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA	3360
	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser	
	1105 1110 1115 1120	
	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT	3408
	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys	
	1125 1130 1135	
	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT	3456
	Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr	
	1140 1145 1150	
	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT	3504
	Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile	
	1155 1160 1165	
	GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA	3552
	Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu	
	1170 1175 1180	
	CTC CTT ATG GAG GAA	3567
	Leu Leu Met Glu Glu	
	1185	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Glu	Asn	Asn	Gln	Asn	Gln	Cys	Ile	Pro	Tyr	Asn	Cys	Leu	Ser
1				5			10						15		

	Asn	Pro	Glu	Glu	Val	Leu	Leu	Asp	Gly	Glu	Arg	Ile	Ser	Thr	Gly	Asn	
				20					25					30			
5	Ser	Ser	Ile	Asp	Ile	Ser	Leu	Ser	Leu	Val	Gln	Phe	Leu	Val	Ser	Asn	
			35				40						45				
	Phe	Val	Pro	Gly	Gly	Gly	Phe	Leu	Val	Gly	Leu	Ile	Asp	Phe	Val	Trp	
		50					55					60					
10	Gly	Ile	Val	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile	Glu	
	65					70				75					80		
	Gln	Leu	Ile	Asn	Glu	Arg	Ile	Ala	Glu	Phe	Ala	Arg	Asn	Ala	Ala	Ile	
15				85					90					95			
	Ala	Asn	Leu	Glu	Gly	Leu	Gly	Asn	Asn	Phe	Asn	Ile	Tyr	Val	Glu	Ala	
			100					105					110				
20	Phe	Lys	Glu	Trp	Glu	Glu	Asp	Pro	Asn	Asn	Pro	Ala	Thr	Arg	Thr	Arg	
			115					120					125				
	Val	Ile	Asp	Arg	Phe	Arg	Ile	Leu	Asp	Gly	Leu	Leu	Glu	Arg	Asp	Ile	
		130					135					140					
25	Pro	Ser	Phe	Arg	Ile	Ser	Gly	Phe	Glu	Val	Pro	Leu	Leu	Ser	Val	Tyr	
	145				150					155					160		
	Ala	Gln	Ala	Ala	Asn	Leu	His	Leu	Ala	Ile	Leu	Arg	Asp	Ser	Val	Ile	
				165					170					175			
30	Phe	Gly	Glu	Ala	Trp	Gly	Leu	Thr	Thr	Ile	Asn	Val	Asn	Glu	Asn	Tyr	
			180					185					190				
35	Asn	Arg	Leu	Ile	Arg	His	Ile	Asp	Glu	Tyr	Ala	Asp	His	Cys	Ala	Asn	
		195					200					205					
	Thr	Tyr	Asn	Arg	Gly	Leu	Asn	Asn	Leu	Pro	Lys	Ser	Thr	Tyr	Gln	Asp	
		210				215						220					
40	Trp	Ile	Thr	Tyr	Asn	Arg	Leu	Arg	Arg	Asp	Leu	Thr	Leu	Thr	Val	Leu	
	225				230					235					240		
	Asp	Ile	Ala	Ala	Phe	Phe	Pro	Asn	Tyr	Asp	Asn	Arg	Arg	Tyr	Pro	Ile	
45				245					250					255			
	Gln	Pro	Val	Gly	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Ile	
			260					265					270				
50	Asn	Phe	Asn	Pro	Gln	Leu	Gln	Ser	Val	Ala	Gln	Leu	Pro	Thr	Phe	Asn	
		275					280						285				
	Val	Met	Glu	Ser	Ser	Ala	Ile	Arg	Asn	Pro	His	Leu	Phe	Asp	Ile	Leu	
		290				295					300						

	Asn	Asn	Leu	Thr	Ile	Phe	Thr	Asp	Trp	Phe	Ser	Val	Gly	Arg	Asn	Phe	
	305					310					315					320	
5	Tyr	Trp	Gly	Gly	His	Arg	Val	Ile	Ser	Ser	Leu	Ile	Gly	Gly	Gly	Asn	
					325					330					335		
	Ile	Thr	Ser	Pro	Ile	Tyr	Gly	Arg	Glu	Ala	Asn	Gln	Glu	Pro	Pro	Arg	
				340					345					350			
10	Ser	Phe	Thr	Phe	Asn	Gly	Pro	Val	Phe	Arg	Thr	Leu	Ser	Asn	Pro	Thr	
				355				360					365				
	Leu	Arg	Leu	Leu	Gln	Gln	Pro	Trp	Pro	Ala	Pro	Pro	Phe	Asn	Leu	Arg	
15		370					375					380					
	Gly	Val	Glu	Gly	Val	Glu	Phe	Ser	Thr	Pro	Thr	Asn	Ser	Phe	Thr	Tyr	
	385					390					395					400	
20	Arg	Gly	Arg	Gly	Thr	Val	Asp	Ser	Leu	Thr	Glu	Leu	Pro	Pro	Glu	Asp	
					405					410					415		
	Asn	Ser	Val	Pro	Pro	Arg	Glu	Gly	Tyr	Ser	His	Arg	Leu	Cys	His	Ala	
				420					425					430			
25	Thr	Phe	Val	Gln	Arg	Ser	Gly	Thr	Pro	Phe	Leu	Thr	Thr	Gly	Val	Val	
			435					440					445				
	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala	Thr	Leu	Thr	Asn	Thr	Ile	Asp	Pro	
	450						455					460					
	Glu	Arg	Ile	Asn	Gln	Ile	Pro	Leu	Val	Lys	Gly	Phe	Arg	Val	Trp	Gly	
	465					470					475					480	
35	Gly	Thr	Ser	Val	Ile	Thr	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	
					485					490					495		
	Arg	Arg	Asn	Thr	Phe	Gly	Asp	Phe	Val	Ser	Leu	Gln	Val	Asn	Ile	Asn	
				500					505					510			
40	Ser	Pro	Ile	Thr	Gln	Arg	Tyr	Arg	Leu	Arg	Phe	Arg	Tyr	Ala	Ser	Ser	
			515					520					525				
	Arg	Asp	Ala	Arg	Val	Ile	Val	Leu	Thr	Gly	Ala	Ala	Ser	Thr	Gly	Val	
45		530					535					540					
	Gly	Gly	Gln	Val	Ser	Val	Asn	Met	Pro	Leu	Gln	Lys	Thr	Met	Glu	Ile	
	545					550					555					560	
50	Gly	Glu	Asn	Leu	Thr	Ser	Arg	Thr	Phe	Arg	Tyr	Thr	Asp	Phe	Ser	Asn	
					565					570					575		
	Pro	Phe	Ser	Phe	Arg	Ala	Asn	Pro	Asp	Ile	Ile	Gly	Ile	Ser	Glu	Gln	
				580					585					590			

	Pro	Leu	Phe	Gly	Ala	Gly	Ser	Ile	Ser	Ser	Gly	Glu	Leu	Tyr	Ile	Asp	
		595						600					605				
5	Lys	Ile	Glu	Ile	Ile	Leu	Ala	Asp	Ala	Thr	Phe	Glu	Ala	Glu	Ser	Asp	
		610					615					620					
	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	Asn	Ala	Leu	Phe	Thr	Ser	Ser	Asn	
	625					630					635					640	
10	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	
				645						650					655		
	Ser	Asn	Leu	Val	Asp	Cys	Leu	Ser	Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	
15				660					665					670			
	Arg	Glu	Leu	Ser	Glu	Lys	Val	Lys	His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	
		675						680					685				
20	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	Phe	Arg	Gly	Ile	Asn	Arg	Gln	Pro	
		690					695					700					
	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	
	705					710					715				720		
25	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	Thr	Leu	Pro	Gly	Thr	Val	Asp	Glu	
				725						730					735		
	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	
				740					745					750			
	Ala	Tyr	Thr	Arg	Tyr	Glu	Leu	Arg	Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	
		755						760					765				
35	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	Asn	Ala	Lys	His	Glu	Ile	Val	Asn	
		770					775					780					
	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	Pro	Leu	Ser	Ala	Gln	Ser	Pro	Ile	
	785					790					795				800		
40	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	
				805						810					815		
	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	Asp	Gly	Glu	Lys	Cys	Ala	His	His	
45			820						825					830			
	Ser	His	His	Phe	Thr	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	
		835						840					845				
50	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	
		850					855					860					
	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Leu	Glu	Glu	Lys	Pro	Leu	Leu	
	865					870					875				880		

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

5 Leu Leu Met Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT	48
Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser	
1 5 10 15	
AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT	96
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	
20 25 30	
TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC	144
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
35 40 45	
TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG	192
Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
50 55 60	
GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA	240
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
65 70 75 80	
CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT	288
Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
85 90 95	
GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA	336
Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
100 105 110	
TTT AAA GAA TGG GAA GAT GAT CCT CAT AAT CCC ACA ACC AGG ACC AGA	384
Phe Lys Glu Trp Glu Asp Asp Pro His Asn Pro Thr Thr Arg Thr Arg	
115 120 125	

	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT	432
	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	
	130 135 140	
5	CCT TCG TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT	480
	Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	
	145 150 155 160	
10	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT	528
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	
	165 170 175	
15	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT	576
	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	
	180 185 190	
20	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT	624
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	
	195 200 205	
25	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT	672
	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp	
	210 215 220	
30	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA	720
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	
	225 230 235 240	
35	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT	768
	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	
	245 250 255	
40	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT	816
	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	
	260 265 270	
45	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC	864
	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	
	275 280 285	
50	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG	912
	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	
	290 295 300	
55	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT	960
	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	
	305 310 315 320	
60	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC	1008
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn	
	325 330 335	

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	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA	1056
	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg	
	340 345 350	
5	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT	1104
	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr	
	355 360 365	
10	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT	1152
	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg	
	370 375 380	
15	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT	1200
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr	
	385 390 395 400	
	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT	1248
	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp	
	405 410 415	
20	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA	1296
	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala	
	420 425 430	
25	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA	1344
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val	
	435 440 445	
30	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA	1392
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	
	450 455 460	
35	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG	1440
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465 470 475 480	
	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT	1488
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
	485 490 495	
40	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT	1536
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	
	500 505 510	
45	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT	1584
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
	515 520 525	
50	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG	1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530 535 540	

	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA	1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545 550 555 560	
5	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT	1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565 570 575	
10	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA	1776
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580 585 590	
15	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT	1824
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595 600 605	
	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT	1872
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610 615 620	
20	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT	1920
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625 630 635 640	
25	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA	1968
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
	645 650 655	
30	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG	2016
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
	660 665 670	
	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG	2064
	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675 680 685	
35	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA	2112
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690 695 700	
40	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT	2160
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705 710 715 720	
45	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG	2208
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
	725 730 735	
50	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA	2256
	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
	740 745 750	

	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC	2304
	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
	755 760 765	
5	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT	2352
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
	770 775 780	
10	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC	2400
	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	
	785 790 795 800	
15	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT	2448
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	
	805 810 815	
20	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT	2496
	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	
	820 825 830	
25	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT	2544
	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	
	835 840 845	
30	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC	2592
	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly	
	850 855 860	
35	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA	2640
	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu	
	865 870 875 880	
40	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC	2688
	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp	
	885 890 895	
45	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA	2736
	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala	
	900 905 910	
50	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA	2784
	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu	
	915 920 925	
55	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT	2832
	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val	
	930 935 940	
60	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT	2880
	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly	
	945 950 955 960	

	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG	2928
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala	
	965 970 975	
5	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT	2976
	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn	
	980 985 990	
10	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG	3024
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	
	995 1000 1005	
15	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA	3072
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu	
	1010 1015 1020	
20	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT	3120
	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	
	1025 1030 1035 1040	
25	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT	3168
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	
	1045 1050 1055	
30	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA	3216
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	
	1060 1065 1070	
35	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG	3264
	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly	
	1075 1080 1085	
40	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT	3312
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr	
	1090 1095 1100	
45	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA	3360
	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser	
	1105 1110 1115 1120	
50	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT	3408
	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys	
	1125 1130 1135	
55	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT	3456
	Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr	
	1140 1145 1150	
60	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT	3504
	Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile	
	1155 1160 1165	

GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA 3552
 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

5 CTC CTT ATG GAG GAA 3567
 Leu Leu Met Glu Glu
 1185

10 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1189 amino acids
 (B) TYPE: amino acid
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

20 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15
 25 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30
 30 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45
 35 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
 50 55 60
 40 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80
 45 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
 85 90 95
 50 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
 100 105 110
 55 Phe Lys Glu Trp Glu Asp Asp Pro His Asn Pro Thr Thr Arg Thr Arg
 115 120 125
 60 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
 130 135 140
 65 Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
 145 150 155 160
 70 Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
 165 170 175

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
 180 185 190
 5 Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
 195 200 205
 Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
 210 215 220
 10 Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
 225 230 235 240
 Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
 245 250 255
 15 Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
 260 265 270
 Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
 275 280 285
 Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
 290 295 300
 20 Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
 305 310 315 320
 Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
 325 330 335
 25 Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
 340 345 350
 Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
 355 360 365
 30 Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
 370 375 380
 35 Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
 385 390 395 400
 Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
 405 410 415
 40 Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
 420 425 430
 Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
 435 440 445
 50 Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
 450 455 460

	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465	475 480
5	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
	485	490 495
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	
	500	505 510
10	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
	515	520 525
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530	535 540
15	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545	550 555 560
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565	570 575
20	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580	585 590
25	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595	600 605
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610	615 620
30	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625	630 635 640
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
	645	650 655
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
	660	665 670
40	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675	680 685
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690	695 700
45	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705	710 715 720
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
	725	730 735
50	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
	740	745 750

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Il His
 1045 1050 1055
 5 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070
 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085
 10 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100
 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120
 15 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135
 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150
 20 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165
 25 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180
 Leu Leu Met Glu Glu
 1185
 30
 35 (2) INFORMATION FOR SEQ ID NO:9:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..3567
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 45 ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT 48
 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15
 50 AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT 96
 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30

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	TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC	144
	Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
	35 40 45	
5	TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG	192
	Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
	50 55 60	
10	GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA	240
	Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
	65 70 75 80	
15	CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT	288
	Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
	85 90 95	
	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA	336
	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
	100 105 110	
	TTT AAA GAA TGG GAA GTA GAT CCT AAT AAT CCT GGA ACC AGG ACC AGA	384
	Phe Lys Glu Trp Glu Val Asp Pro Asn Asn Pro Gly Thr Arg Thr Arg	
	115 120 125	
	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT	432
	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	
	130 135 140	
	CCT TCG TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT	480
	Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	
	145 150 155 160	
35	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT	528
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	
	165 170 175	
	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT	576
	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	
	180 185 190	
40	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT	624
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	
	195 200 205	
45	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT	672
	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp	
	210 215 220	
50	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA	720
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	
	225 230 235 240	

GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT 768
 Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
 245 250 255

5 CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT 816
 Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
 260 265 270

10 AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC 864
 Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
 275 280 285

15 GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG 912
 Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
 290 295 300

20 AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT 960
 Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
 305 310 315 320

25 TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC 1008
 Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
 325 330 335

30 ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA 1056
 Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
 340 345 350

35 TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT 1104
 Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
 355 360 365

40 TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT 1152
 Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
 370 375 380

45 GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT 1200
 Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
 385 390 395 400

50 CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT 1248
 Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
 405 410 415

45 AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA 1296
 Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
 420 425 430

50 ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA 1344
 Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
 435 440 445

	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA	1392
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	
	450 455 460	
5	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG	1440
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465 470 475 480	
10	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT	1488
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
	485 490 495	
15	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT	1536
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	
	500 505 510	
	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT	1584
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
	515 520 525	
20	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG	1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530 535 540	
25	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA	1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545 550 555 560	
30	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT	1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565 570 575	
35	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA	1776
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580 585 590	
40	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT	1824
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595 600 605	
	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT	1872
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610 615 620	
45	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT	1920
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625 630 635 640	
50	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA	1968
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
	645 650 655	

	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG	2016
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
	660 665 670	
5	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG	2064
	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675 680 685	
10	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA	2112
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690 695 700	
15	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT	2160
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705 710 715 720	
20	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG	2208
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
	725 730 735	
25	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA	2256
	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
	740 745 750	
30	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC	2304
	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
	755 760 765	
35	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT	2352
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
	770 775 780	
40	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC	2400
	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	
	785 790 795 800	
45	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT	2448
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	
	805 810 815	
50	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT	2496
	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	
	820 825 830	
55	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT	2544
	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	
	835 840 845	
60	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC	2592
	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly	
	850 855 860	

	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA	2640
	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu	
	865 870 875 880	
5	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC	2688
	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp	
	885 890 895	
10	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA	2736
	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala	
	900 905 910	
15	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA	2784
	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu	
	915 920 925	
20	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT	2832
	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val	
	930 935 940	
25	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT	2880
	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly	
	945 950 955 960	
30	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG	2928
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala	
	965 970 975	
35	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT	2976
	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn	
	980 985 990	
40	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG	3024
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	
	995 1000 1005	
45	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA	3072
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu	
	1010 1015 1020	
50	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT	3120
	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	
	1025 1030 1035 1040	
55	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT	3168
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	
	1045 1050 1055	
60	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA	3216
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	
	1060 1065 1070	

GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG 3264
 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085

5 ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT 3312
 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100

10 GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA 3360
 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120

15 GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT 3408
 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135

GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT 3456
 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150

20 GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT 3504
 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

25 GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA 3552
 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

30 CTC CTT ATG GAG GAA 3567
 Leu Leu Met Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO:10:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1189 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

45 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15
 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30
 50 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45

	Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
	50 55 60	
5	Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
	65 70 75 80	
	Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
	85 90 95	
10	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
	100 105 110	
	Phe Lys Glu Trp Glu Val Asp Pro Asn Asn Pro Gly Thr Arg Thr Arg	
	115 120 125	
15	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	
	130 135 140	
	Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	
20	145 150 155 160	
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	
	165 170 175	
25	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	
	180 185 190	
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	
	195 200 205	
30	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp	
	210 215 220	
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	
35	225 230 235 240	
	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	
	245 250 255	
40	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	
	260 265 270	
	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	
	275 280 285	
45	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	
	290 295 300	
	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	
50	305 310 315 320	
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn	
	325 330 335	

Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
 340 345 350
 5 Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
 355 360 365
 Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
 370 375 380
 10 Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
 385 390 395 400
 Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
 405 410 415
 15 Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
 420 425 430
 Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
 435 440 445
 20 Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
 450 455 460
 25 Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
 465 470 475 480
 Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
 485 490 495
 30 Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn
 500 505 510
 35 Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
 515 520 525
 Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
 530 535 540
 40 Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
 545 550 555 560
 Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
 565 570 575
 45 Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
 580 585 590
 50 Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
 595 600 605
 Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
 610 615 620

Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
 625 630 635 640
 5 Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
 645 650 655
 Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
 660 665 670
 10 Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
 675 680 685
 Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
 690 695 700
 15 Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
 705 710 715 720
 20 Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
 725 730 735
 Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
 740 745 750
 25 Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
 755 760 765
 Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
 770 775 780
 30 Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
 785 790 795 800
 35 Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
 805 810 815
 Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
 820 825 830
 40 Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
 835 840 845
 Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
 850 855 860
 45 His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
 865 870 875 880
 Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
 885 890 895
 50 Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
 900 905 910

Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
 915 920 925
 5 Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
 930 935 940
 His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
 945 950 955 960
 10 Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
 965 970 975
 Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
 980 985 990
 15 Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
 995 1000 1005
 Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
 1010 1015 1020
 Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1025 1030 1035 1040
 20 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055
 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070
 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085
 25 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100
 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120
 40 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135
 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150
 45 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165
 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 50 1170 1175 1180
 Leu Leu Met Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT	48
Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser	
1 5 10 15	
AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT	96
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	
20 25 30	
TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC	144
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
35 40 45	
TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG	192
Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
50 55 60	
GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA	240
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
65 70 75 80	
CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT	288
Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
85 90 95	
GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA	336
Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
100 105 110	
TTT AAA GAA TGG GAA GAA GAT CCC CAT AAT CCA GCA ACC AGG ACC AGA	384
Phe Lys Glu Trp Glu Glu Asp Pro His Asn Pro Ala Thr Arg Thr Arg	
115 120 125	
GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT	432
Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	
130 135 140	
CCT TCG TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT	480
Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	
145 150 155 160	

	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT	528
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	
	165 170 175	
5	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT	576
	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	
	180 185 190	
10	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT	624
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	
	195 200 205	
15	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT	672
	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp	
	210 215 220	
20	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA	720
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	
	225 230 235 240	
25	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT	768
	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	
	245 250 255	
30	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT	816
	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	
	260 265 270	
35	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC	864
	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	
	275 280 285	
40	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG	912
	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	
	290 295 300	
45	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT	960
	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	
	305 310 315 320	
50	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC	1008
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn	
	325 330 335	
55	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA	1056
	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg	
	340 345 350	
60	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT	1104
	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr	
	355 360 365	

	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT	1152
	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg	
	370 375 380	
5	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT	1200
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr	
	385 390 395 400	
10	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT	1248
	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp	
	405 410 415	
15	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA	1296
	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala	
	420 425 430	
20	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA	1344
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val	
	435 440 445	
25	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA	1392
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	
	450 455 460	
30	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG	1440
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465 470 475 480	
35	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT	1488
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
	485 490 495	
40	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT	1536
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	
	500 505 510	
45	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT	1584
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
	515 520 525	
50	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG	1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530 535 540	
55	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA	1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545 550 555 560	
60	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT	1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565 570 575	

	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA	1776
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580 585 590	
5	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT	1824
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595 600 605	
10	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT	1872
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610 615 620	
15	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT	1920
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625 630 635 640	
20	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA	1968
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
	645 650 655	
25	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG	2016
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
	660 665 670	
30	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG	2064
	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675 680 685	
35	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA	2112
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690 695 700	
40	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT	2160
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705 710 715 720	
45	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG	2208
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
	725 730 735	
50	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA	2256
	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
	740 745 750	
55	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC	2304
	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
	755 760 765	
60	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT	2352
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
	770 775 780	

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	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG	3024
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	
	995 1000 1005	
5	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA	3072
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu	
	1010 1015 1020	
10	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT	3120
	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	
	1025 1030 1035 1040	
15	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT	3168
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	
	1045 1050 1055	
	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA	3216
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	
	1060 1065 1070	
20	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG	3264
	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly	
	1075 1080 1085	
25	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT	3312
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr	
	1090 1095 1100	
30	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA	3360
	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser	
	1105 1110 1115 1120	
	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT	3408
	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys	
	1125 1130 1135	
	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT	3456
	Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr	
	1140 1145 1150	
40	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT	3504
	Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile	
	1155 1160 1165	
45	GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA	3552
	Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu	
	1170 1175 1180	
50	CTC CTT ATG GAG GAA	3567
	Leu Leu Met Glu Glu	
	1185	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
1 5 10 15

Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
20 25 30

Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
35 40 45

Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
50 55 60

Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65 70 75 80

Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
85 90 95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
100 105 110

Phe Lys Glu Trp Glu Glu Asp Pro His Asn Pro Ala Thr Arg Thr Arg
115 120 125

Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
130 135 140

Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145 150 155 160

Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
165 170 175

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
180 185 190

Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
195 200 205

Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
210 215 220

Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
225 230 235 240

Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
 245 250 255
 5 Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
 260 265 270
 Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
 275 280 285
 10 Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
 290 295 300
 Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
 15 305 310 315 320
 Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
 325 330 335
 20 Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
 340 345 350
 Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
 355 360 365
 25 Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
 370 375 380
 Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
 385 390 395 400
 Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
 405 410 415
 35 Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
 420 425 430
 Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
 435 440 445
 40 Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
 450 455 460
 Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
 45 465 470 475 480
 Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
 485 490 495
 50 Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn
 500 505 510
 Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
 515 520 525

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	Arg	Asp	Ala	Arg	Val	Ile	Val	Leu	Thr	Gly	Ala	Ala	Ser	Thr	Gly	Val
	530						535						540			
5	Gly	Gly	Gln	Val	Ser	Val	Asn	Met	Pro	Leu	Gln	Lys	Thr	Met	Glu	Ile
	545					550				555					560	
	Gly	Glu	Asn	Leu	Thr	Ser	Arg	Thr	Phe	Arg	Tyr	Thr	Asp	Phe	Ser	Asn
				565					570					575		
10	Pro	Phe	Ser	Phe	Arg	Ala	Asn	Pro	Asp	Ile	Ile	Gly	Ile	Ser	Glu	Gln
				580				585						590		
	Pro	Leu	Phe	Gly	Ala	Gly	Ser	Ile	Ser	Ser	Gly	Glu	Leu	Tyr	Ile	Asp
15			595				600					605				
	Lys	Ile	Glu	Ile	Ile	Leu	Ala	Asp	Ala	Thr	Phe	Glu	Ala	Glu	Ser	Asp
	610					615					620					
20	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	Asn	Ala	Leu	Phe	Thr	Ser	Ser	Asn
	625					630					635					640
	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	Thr	Asp	Tyr	His	Ile	Asp	Gln	Val
				645					650					655		
25	Ser	Asn	Leu	Val	Asp	Cys	Leu	Ser	Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys
			660					665					670			
	Arg	Glu	Leu	Ser	Glu	Lys	Val	Lys	His	Ala	Lys	Arg	Leu	Ser	Asp	Glu
		675					680						685			
	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	Phe	Arg	Gly	Ile	Asn	Arg	Gln	Pro
		690					695				700					
35	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp
	705					710					715				720	
	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	Thr	Leu	Pro	Gly	Thr	Val	Asp	Glu
				725						730					735	
40	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys
				740					745					750		
	Ala	Tyr	Thr	Arg	Tyr	Glu	Leu	Arg	Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp
45			755					760					765			
	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	Asn	Ala	Lys	His	Glu	Ile	Val	Asn
		770					775					780				
50	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	Pro	Leu	Ser	Ala	Gln	Ser	Pro	Ile
	785					790					795					800
	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro	His	Leu	Glu	Trp	Asn
				805						810					815	

	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	820	825	830
5	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	835	840	845
	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly	850	855	860
10	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu	865	870	875 880
	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp	885	890	895
15	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala	900	905	910
	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu	915	920	925
20	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val	930	935	940
	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly	945	950	955 960
25	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala	965	970	975
	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn	980	985	990
30	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	995	1000	1005
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu	1010	1015	1020
35	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	1025	1030	1035 1040
40	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	1045	1050	1055
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	1060	1065	1070
45	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly	1075	1080	1085
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr	1090	1095	1100

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120

5 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150

10 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

15 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

Leu Leu Met Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCATTAAAG AATGGGAAGA AGATAATAAT CCAGCAACCA GGACCAGAG

49

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCATTAAAG AATGGGAAGA AGATCCTAAT GCAAATCCAG CAACCAGGAC CAGAG

55

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCGATCGGC CGCATGC

17

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCATTTAAAG AATGGGAAGG GATCCTAGGA ATCCAGCAAC CAGGACCAGA G

51

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAGCTCTTGT TAAAAAAGGT GTTCCAGATC

30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 19..39
- (D) OTHER INFORMATION: /note= "N = G, A, T or C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCATTTAAAG AATGGGAANN NNNNNNNNNN NNNNNNNNNA CCAGGACCAG AGTAATTGAT

60

CG

62

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGGCTACTTG AAAGGGACAT TCCTTCGTTT GCAATTTCTG GATTGAAGT ACCCC

55

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCAAGAAAAT ACTAGAGCTC TTGTTAAAAA AGGTGTTCC

39

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTCTGT AATTTTTGGA GAAGCATGGG GGTGACAAC GATAAATGTC

50

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCATTTAAAG AATGGGAAGA AGATCCTAAT AATCCAGCAA CCAGGACCAG AGTAATTGAT

60

CGC

63

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu Asp Pro Asn Asn Pro Ala
1 5

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATTTAAAG AATGGGAAGG GATCCTAGGA ATCCAGCAAC CAGGACCAGA G

51

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCATTTAAAG AATGGGAAGA TGATCCTCAT AATCCCACAA CCAGGACCAG AGTAATTGAT

60

CGC

63

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Asp Asp Pro His Asn Pro Thr
1 5

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Val Asp Pro Asn Asn Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met
1 5 10 15
Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Leu Ala Val Gln Asn Tyr
20 25 30
Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45
Ser Val
50

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr Asn Pro Ala Leu Thr Glu Glu Met Arg Ile Gln Phe Asn Asp Met
1 5 10 15
Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Phe Thr Val Gln Asn Tyr
20 25 30

Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
 35 40 45

Ser Val
 50

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met
 1 5 10 15

Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Phe Ala Val Gln Asn Tyr
 20 25 30

Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
 35 40 45

Ser Val
 50

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met
 1 5 10 15

Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Phe Thr Val Gln Asn Tyr
 20 25 30

Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Val Asn Leu His Leu
 35 40 45

Ser Val
 50

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met
1 5 10 15

Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Phe Ala Val Gln Asn Tyr
20 25 30

Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45

Ser Val
50

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asn Asn Ala Gln Leu Arg Glu Asp Val Arg Ile Arg Phe Ala Asn Thr
1 5 10 15

Asp Asp Ala Leu Ile Thr Ala Ile Asn Asn Phe Thr Leu Thr Ser Phe
20 25 30

Glu Ile Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45

Ser Leu
50

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asn Asn Ala Gln Leu Arg Glu Asp Val Arg Ile Arg Phe Ala Asn Thr
1 5 10 15

Asp Asp Ala Leu Ile Thr Ala Ile Asn Asn Phe Thr Leu Thr Ser Phe
20 25 30

Glu Ile Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45

Ser Leu
50

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asn Asn Pro Ala Ser Gln Glu Arg Val Arg Thr Arg Phe Arg Leu Thr
1 5 10 15

Asp Asp Ala Ile Val Thr Gly Leu Pro Thr Leu Ala Ile Arg Asn Leu
20 25 30

Glu Val Val Asn Leu Ser Val Tyr Thr Gln Ala Ala Asn Leu His Leu
35 40 45

Ser Leu
50

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Asn Asn Pro Glu Thr Arg Thr Arg Val Ile Asp Arg Phe Arg Ile Leu
1 5 10 15

Asp Gly Leu Leu Glu Arg Asp Ile Pro Ser Phe Arg Ile Ser Gly Phe
20 25 30

Glu Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu
 35 40 45

Ala Ile
 50

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asp Asn Pro Val Thr Arg Thr Arg Val Val Asp Arg Phe Arg Ile Leu
 1 5 10 15
 Asp Gly Leu Leu Glu Arg Asp Ile Pro Ser Phe Arg Ile Ala Gly Phe
 20 25 30
 Glu Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu
 35 40 45
 Ala Ile
 50

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Thr Asn Pro Ala Leu Lys Glu Glu Met Arg Thr Gln Phe Asn Asp Met
 1 5 10 15
 Asn Ser Ile Leu Val Thr Ala Ile Pro Leu Phe Ser Val Gln Asn Tyr
 20 25 30
 Gln Val Pro Phe Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
 35 40 45
 Ser Val
 50

(2) INFORMATION FOR SEQ ID NO:39:

Glu Ile Pro Leu Leu Thr Val Tyr Val Gln Ala Ala Asn Leu His Leu
 35 40 45

Ser Leu
 50

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asp Asn Glu Ala Ala Lys Ser Arg Val Ile Asp Arg Phe Arg Ile Leu
 1 5 10 15
 Asp Gly Leu Ile Glu Ala Asn Ile Pro Ser Phe Arg Ile Ile Gly Phe
 20 25 30
 Glu Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
 35 40 45
 Ala Leu
 50

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Asp Asn Thr Ala Ala Arg Ser Arg Val Thr Glu Arg Phe Arg Ile Ile
 1 5 10 15
 Asp Ala Gln Ile Glu Ala Asn Ile Pro Ser Phe Arg Ile Pro Gly Phe
 20 25 30
 Glu Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu
 35 40 45
 Ala Leu
 50

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Asp Asp Ala Arg Thr Arg Ser Val Leu Tyr Thr Gln Tyr Ile Ala Leu
1 5 10 15
Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn Gln
20 25 30
Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45
Leu Leu
50

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val Ala Leu
1 5 10 15
Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg Asn Glu
20 25 30
Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45
Leu Leu
50

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val Ala Leu
1 5 10 15

Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg Asn Glu
20 25 30

Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45

Leu Leu
50

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asn Asp Ala Arg Ser Arg Ser Ile Ile Arg Glu Arg Tyr Ile Ala Leu
1 5 10 15

Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Ser Ile Arg Asn Glu
20 25 30

Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45

Leu Leu
50

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser Gln Tyr Ile Ala Leu
1 5 10 15

Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe Ala Val Ser Gly Glu
20 25 30

Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala Ala Asn Leu His Leu
 35 40 45
 Leu Leu
 50

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Asn Asn Thr Arg Ala Arg Ser Val Val Lys Asn Gln Tyr Ile Ala Leu
 1 5 10 15
 Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe Ala Val Ser Gly Glu
 20 25 30
 Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala Ala Asn Leu His Leu
 35 40 45
 Leu Leu
 50

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGATCCCTCG AGCTGCAGGA GC

22

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
 (B) LOCATION: 31..33

(D) OTHER INFORMATION: /note= "N = C, A, T or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

5 GGGCTACTTG AAAGGGACAT TCCTTCGTTT NNNATTCTG GATTGAAGT ACCCC 55

(2) INFORMATION FOR SEQ ID NO:54:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCATTTAAAG AATGGGAAGT AGATCCTAAT AATCCTGGAA CCAGGACCAG AGTAATTGAT 60

20 CGC 63

(2) INFORMATION FOR SEQ ID NO:55:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Val Asp Pro Asn Asn Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:56:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCATTTAAAG AATGGGAAGA AGATCCCCAT AATCCAGCAA CCAGGACCAG AGTAATTGAT 60

50 CGC 63

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Glu Asp Pro His Asn Pro Ala
1 5

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT	48
Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser	
1 5 10 15	
AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT	96
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	
20 25 30	
TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC	144
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
35 40 45	
TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG	192
Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
50 55 60	
GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA	240
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
65 70 75 80	
CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT	288
Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
85 90 95	
GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA	336
Ala Asn Leu Glu Gly Leu Gly Asn Phe Asn Ile Tyr Val Glu Ala	
100 105 110	

	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA	384
	Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg	
	115 120 125	
5	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT	432
	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	
	130 135 140	
10	CCT TCG TTT GCA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT	480
	Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	
	145 150 155 160	
15	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT	528
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	
	165 170 175	
20	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT	576
	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	
	180 185 190	
25	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT	624
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	
	195 200 205	
30	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG GCT AGC ACG TAT CAA GAT	672
	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Ala Ser Thr Tyr Gln Asp	
	210 215 220	
35	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA	720
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	
	225 230 235 240	
40	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT	768
	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	
	245 250 255	
45	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT	816
	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	
	260 265 270	
50	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC	864
	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	
	275 280 285	
55	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG	912
	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	
	290 295 300	
60	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT	960
	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	
	305 310 315 320	

	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG	1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530 535 540	
5	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA	1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545 550 555 560	
10	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT	1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565 570 575	
15	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA	1776
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580 585 590	
	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT	1824
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595 600 605	
20	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT	1872
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610 615 620	
25	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT	1920
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625 630 635 640	
30	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA	1968
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
	645 650 655	
35	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG	2016
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
	660 665 670	
40	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG	2064
	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675 680 685	
	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA	2112
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690 695 700	
45	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT	2160
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705 710 715 720	
50	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG	2208
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
	725 730 735	

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	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA	2256
	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
	740 745 750	
5	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC	2304
	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
	755 760 765	
10	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT	2352
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
	770 775 780	
15	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC	2400
	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	
	785 790 795 800	
	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT	2448
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	
	805 810 815	
20	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT	2496
	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	
	820 825 830	
25	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT	2544
	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	
	835 840 845	
30	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC	2592
	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly	
	850 855 860	
35	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA	2640
	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu	
	865 870 875 880	
40	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC	2688
	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp	
	885 890 895	
45	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA	2736
	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala	
	900 905 910	
50	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT	2832
	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val	
	930 935 940	

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	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT	2880
	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly	
	945 950 955 960	
5	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG	2928
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala	
	965 970 975	
10	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT	2976
	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn	
	980 985 990	
15	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG	3024
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	
	995 1000 1005	
	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA	3072
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu	
	1010 1015 1020	
	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT	3120
	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	
	1025 1030 1035 1040	
25	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT	3168
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	
	1045 1050 1055	
30	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA	3216
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	
	1060 1065 1070	
35	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG	3264
	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly	
	1075 1080 1085	
40	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT	3312
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr	
	1090 1095 1100	
	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA	3360
	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser	
	1105 1110 1115 1120	
45	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT	3408
	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys	
	1125 1130 1135	
50	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT	3456
	Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr	
	1140 1145 1150	

GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT 3504
 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

5 GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA 3552
 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

10 CTC CTT ATG GAG GAA 3567
 Leu Leu Met Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15

Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30

Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45

Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
 50 55 60

Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80

40 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
 85 90 95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
 100 105 110

45 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
 115 120 125

50 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
 130 135 140

Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
 145 150 155 160

Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
 165 170 175
 5 Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
 180 185 190
 Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
 195 200 205
 10 Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Ala Ser Thr Tyr Gln Asp
 210 215 220
 Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
 225 230 235 240
 15 Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
 245 250 255
 Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
 260 265 270
 Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
 275 280 285
 20 Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
 290 295 300
 Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
 305 310 315 320
 25 Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
 325 330 335
 Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
 340 345 350
 30 Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
 355 360 365
 35 Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
 370 375 380
 Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
 385 390 395 400
 40 Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
 405 410 415
 45 Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
 420 425 430
 50 Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
 435 440 445

	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala	Thr	Leu	Thr	Asn	Thr	Ile	Asp	Pro	
	450						455					460					
5	Glu	Arg	Ile	Asn	Gln	Ile	Pro	Leu	Val	Lys	Gly	Phe	Arg	Val	Trp	Gly	
	465					470					475					480	
	Gly	Thr	Ser	Val	Ile	Thr	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	
					485					490					495		
10	Arg	Arg	Asn	Thr	Phe	Gly	Asp	Phe	Val	Ser	Leu	Gln	Val	Asn	Ile	Asn	
				500					505					510			
	Ser	Pro	Ile	Thr	Gln	Arg	Tyr	Arg	Leu	Arg	Phe	Arg	Tyr	Ala	Ser	Ser	
			515					520					525				
15	Arg	Asp	Ala	Arg	Val	Ile	Val	Leu	Thr	Gly	Ala	Ala	Ser	Thr	Gly	Val	
	530					535				540							
	Gly	Gly	Gln	Val	Ser	Val	Asn	Met	Pro	Leu	Gln	Lys	Thr	Met	Glu	Ile	
20	545				550				555						560		
	Gly	Glu	Asn	Leu	Thr	Ser	Arg	Thr	Phe	Arg	Tyr	Thr	Asp	Phe	Ser	Asn	
				565					570					575			
25	Pro	Phe	Ser	Phe	Arg	Ala	Asn	Pro	Asp	Ile	Ile	Gly	Ile	Ser	Glu	Gln	
				580				585					590				
	Pro	Leu	Phe	Gly	Ala	Gly	Ser	Ile	Ser	Ser	Gly	Glu	Leu	Tyr	Ile	Asp	
			595				600					605					
30	Lys	Ile	Glu	Ile	Ile	Leu	Ala	Asp	Ala	Thr	Phe	Glu	Ala	Glu	Ser	Asp	
	610				615				620								
	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	Asn	Ala	Leu	Phe	Thr	Ser	Ser	Asn	
	625				630				635					640			
	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	
				645					650				655				
40	Ser	Asn	Leu	Val	Asp	Cys	Leu	Ser	Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	
			660						665				670				
	Arg	Glu	Leu	Ser	Glu	Lys	Val	Lys	His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	
			675				680					685					
45	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	Phe	Arg	Gly	Ile	Asn	Arg	Gln	Pro	
			690			695					700						
	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	
50	705				710				715				720				
	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	Thr	Leu	Pro	Gly	Thr	Val	Asp	Glu	
				725					730				735				

	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	
				740					745					750			
5	Ala	Tyr	Thr	Arg	Tyr	Glu	Leu	Arg	Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	
				755				760					765				
	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	Asn	Ala	Lys	His	Glu	Ile	Val	Asn	
		770					775					780					
10	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	Pro	Leu	Ser	Ala	Gln	Ser	Pro	Ile	
	785					790				795					800		
	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	
				805						810					815		
15	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	Asp	Gly	Glu	Lys	Cys	Ala	His	His	
			820						825					830			
	Ser	His	His	Phe	Thr	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	
			835					840					845				
	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	
		850					855					860					
25	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Leu	Glu	Glu	Lys	Pro	Leu	Leu	
	865					870					875				880		
	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	
				885						890					895		
30	Lys	Arg	Glu	Lys	Leu	Gln	Leu	Glu	Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	
			900						905					910			
	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe	Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	
		915						920				925					
	Gln	Val	Asp	Thr	Asn	Ile	Ala	Met	Ile	His	Ala	Ala	Asp	Lys	Arg	Val	
		930					935					940					
40	His	Arg	Ile	Arg	Glu	Ala	Tyr	Leu	Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	
	945					950				955					960		
	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu	Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	
				965					970					975			
45	Tyr	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	
			980					985					990				
	Asn	Gly	Leu	Leu	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Glu	Glu	
50			995				1000					1005					
	Gln	Asn	Asn	His	Arg	Ser	Val	Leu	Val	Ile	Pro	Glu	Trp	Glu	Ala	Glu	
		1010					1015					1020					

Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1025 1030 1035 1040

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055

Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070

Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120

Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150

Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

Leu Leu Met Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT
 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15

48

	AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT	96
	Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	
	20 25 30	
5	TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC	144
	Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
	35 40 45	
10	TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG	192
	Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
	50 55 60	
15	GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA	240
	Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
	65 70 75 80	
	CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT	288
	Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
	85 90 95	
20	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA	336
	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
	100 105 110	
25	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA	384
	Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg	
	115 120 125	
30	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT	432
	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	
	130 135 140	
35	CCT TCG TTT GAC ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT	480
	Pro Ser Phe Asp Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	
	145 150 155 160	
40	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT	528
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	
	165 170 175	
45	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT	576
	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	
	180 185 190	
50	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT	624
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	
	195 200 205	
55	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG GCT AGC ACG TAT CAA GAT	672
	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Ala Ser Thr Tyr Gln Asp	
	210 215 220	

	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA	1344
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val	
	435 440 445	
5	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA	1392
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	
	450 455 460	
10	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG	1440
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465 470 475 480	
15	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT	1488
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
	485 490 495	
	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT	1536
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	
	500 505 510	
20	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT	1584
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
	515 520 525	
25	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG	1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530 535 540	
30	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA	1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545 550 555 560	
35	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT	1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565 570 575	
40	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA	1776
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580 585 590	
	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT	1824
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595 600 605	
45	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT	1872
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610 615 620	
50	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT	1920
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625 630 635 640	

	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA	1968
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
	645 650 655	
5	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG	2016
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
	660 665 670	
10	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG	2064
	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675 680 685	
15	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA	2112
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690 695 700	
20	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT	2160
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705 710 715 720	
25	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG	2208
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
	725 730 735	
30	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA	2256
	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
	740 745 750	
35	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC	2304
	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
	755 760 765	
40	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT	2352
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
	770 775 780	
45	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC	2400
	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	
	785 790 795 800	
50	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT	2448
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	
	805 810 815	
55	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT	2496
	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	
	820 825 830	
60	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT	2544
	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	
	835 840 845	

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	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA	3216
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	
	1060 1065 1070	
5	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG	3264
	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly	
	1075 1080 1085	
10	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT	3312
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr	
	1090 1095 1100	
15	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA	3360
	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser	
	1105 1110 1115 1120	
	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT	3408
	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys	
	1125 1130 1135	
	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT	3456
	Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr	
	1140 1145 1150	
25	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT	3504
	Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile	
	1155 1160 1165	
30	GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA	3552
	Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu	
	1170 1175 1180	
	CTC CTT ATG GAG GAA	3567
	Leu Leu Met Glu Glu	
	1185	

(2) INFORMATION FOR SEQ ID NO:61:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1189 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

50	Met	Glu	Glu	Asn	Asn	Gln	Asn	Gln	Cys	Ile	Pro	Tyr	Asn	Cys	Leu	Ser
	1			5				10						15		
	Asn	Pro	Glu	Glu	Val	Leu	Leu	Asp	Gly	Glu	Arg	Ile	Ser	Thr	Gly	Asn
			20					25						30		

Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45
 Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
 5 50 55 60
 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80
 10 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
 85 90 95
 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
 100 105 110
 15 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
 115 120 125
 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
 130 135 140
 Pro Ser Phe Asp Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
 145 150 155 160
 25 Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
 165 170 175
 Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
 180 185 190
 30 Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
 195 200 205
 Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Ala Ser Thr Tyr Gln Asp
 210 215 220
 Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
 225 230 235 240
 40 Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
 245 250 255
 Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
 260 265 270
 45 Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
 275 280 285
 Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
 290 295 300
 50 Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
 305 310 315 320

	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn	
	325	330 335
5	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg	
	340	345 350
	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr	
	355	360 365
10	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg	
	370	375 380
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr	
	385	390 395 400
15	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp	
	405	410 415
20	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala	
	420	425 430
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val	
	435	440 445
25	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	
	450	455 460
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465	470 475 480
30	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
	485	490 495
35	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	
	500	505 510
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
	515	520 525
40	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530	535 540
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545	550 555 560
45	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565	570 575
50	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580	585 590
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595	600 605

Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
 610 615 620

5 Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
 625 630 635 640

Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
 645 650 655

10 Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
 660 665 670

Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
 675 680 685

15 Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
 690 695 700

20 Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
 705 710 715 720

Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
 725 730 735

25 Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
 740 745 750

30 Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
 755 760 765

35 Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
 770 775 780

Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
 785 790 795 800

Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
 805 810 815

40 Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
 820 825 830

Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
 835 840 845

45 Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
 850 855 860

50 His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
 865 870 875 880

Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
 885 890 895

Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
 900 905 910

5 Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
 915 920 925

Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
 930 935 940

10 His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
 945 950 955 960

Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
 965 970 975

15 Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
 980 985 990

20 Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
 995 1000 1005

Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
 1010 1015 1020

25 Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1025 1030 1035 1040

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055

30 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070

35 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100

40 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120

Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135

45 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150

50 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

Leu Leu Met Glu Glu
1185

5 (2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

15 CGGGGATTAA ATAATTTACC GGCTAGCACG TATCAAGATT GGATAAC

47

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CGGGGATTAA ATAATTTACC GAAAAACGTA TCAAGATTGG ATAAC

45

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGATAGCACT CATCAAAGGT ACC

23

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CGGGGATTAA ATAATACCGA AAAGCACGTA TCAAGATTGG ATAAC

45

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CGGGGATTAA ATAATTTAAA AAAGCACGTA TCAAGATTGG ATAAC

45

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CGGGGATTAA ATAATTTACC GAAGCACGTA TCAAGATTGG ATAAC

45

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGATTAAATA ATTTACCGAA AAGCATATCA AGATTGGATA ACATATAATC G

51

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGATTAAATA ATTTACCGAA AAGCACGACA AGATTGGATA ACATATAATC G

51

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GATTCTGTAA TTTTGTAGAAA GATGGGGATT GACAACGATA AATGTCAATG

50

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GATTCTGTAA TTTTGTGAAA GATGGGGATT GACAACGATA AATGTCAATG

50

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATTCTGTAA TTTTGTGAGA AATGGGGATT GACAACGATA AATGTCAATG

50

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TCTGTAATTT TTGGAGAAAG AAGGATTGAC AACGATAAAT GTCAATGAAA AC

52

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTAATTTTGTG GAGAAAGATG GATTGACAAC GATAAATGTC AATGAAAAC

49

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GTAATTTTGTG GAGAAAGATG GGGAAACAAC GATAAATGTC AATGAAAAC

49

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GTAATTTTGTG GAGAAAGATG GGGATTGAAC GATAAATGTC AATGAAAAC

49